

Petri Nets and Bio-Modelling

and how to benefit from their synergy

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Petri nets are a general, well-established model of concurrent and distributed computation featuring a wealth of tools for the analysis and verification of their behavioural properties. On the other hand, to understand specific biological processes different formalisations have been proposed. Examples here are membrane systems and reaction systems which are close abstractions of the functioning of the living cell. Membrane systems are a computational model inspired by the way chemical reactions take place in cells that are divided by membranes into compartments. The central idea behind reaction systems is that the functioning of a living cell is based on interactions between (a large number of) individual reactions, and moreover these interactions are regulated by two main mechanisms: facilitation and inhibition.

In this talk we are concerned with the intrinsic similarities and differences between Petri nets on the one hand, and membrane systems and reaction systems on the other hand. In particular, we are interested in the benefits that can result from establishing strong semantical links between the latter two models and Petri nets. Our aim is to enhance the Petri net model in order to faithfully model the dynamics of the biological phenomena/processes represented by membrane systems and reaction systems.

After introducing Petri nets, we will outline how to understand and formalise their causality and concurrency semantics.

Then we turn to membrane systems. Like membrane systems, Petri nets are in essence multiset rewriting systems. Using this key commonality we describe a faithful translation from basic membrane systems to Petri nets. To capture the compartmentalisation of membrane systems, the Petri net model has to be extended with localities which in turn leads to the idea of locally synchronised executions. In the thus extended model the standard causality semantics is no longer sound, and we will discuss possible solution to this problem.

Next we describe reaction systems which are a recently proposed model aimed at investigating processes carried by biochemical reactions. Now, the resulting computational model is remarkably different since in reaction systems, biochemical reactions are modeled using a qualitative rather than a quantitative approach. As a consequence, counting — and hence the multiset based calculus implemented in Petri nets — is no longer appropriate. This insight leads to a new class of Petri nets, called set-nets, a novel and challenging class of nets with intriguing (and yet to be discovered) properties.

We conclude the talk by demonstrating how in turn set-nets with localities correspond to membrane systems with qualitative evolution rules.

Altogether this talk aims to demonstrate the fruitful two-way interaction between biological models and Petri nets. Both membrane systems and reaction systems have inspired the introduction of new and

relevant extensions to the basic net model, whereas having a Petri net semantics opens the way for a new understanding, analysis and synthesis techniques for biologically inspired systems.

The presentation is essentially self-contained; in particular, all the necessary details concerning the three models will be provided.

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